Must be sent with the out going letter, No Exceptions.

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

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Source:

Date Processed by STIC:

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FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

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http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

- 1. EFS-Bio (http://www.uspto.gov/ebc/efs/downloads/documents.htm, EFS Submission User Manual ePAVE)
- 2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
- 3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
 U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street,
 Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 0593,659
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
IWrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3Misaligned Amino Numbering	The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5Variable Length	Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6PatentIn 2.0 "bug"	sequences(s) Normally, previously coded nucleic acid sequence	Patentin would automatically generate this section from the Please manually copy the relevant <220>-<223> section to This applies to the mandatory <220>-<223> sections for
7Skipped Sequences (OLD RULES)	(2) INFORMATION FOR SEQ ID NO (i) SEQUENCE CHARACTER	onal, please insert the following lines for each skipped sequence: 2:X: (insert SEQ ID NO where "X" is shown) USTICS: (Do not insert any subheadings under this heading) 2: ID NO:X: (insert SEQ ID NO where "X" is shown)
	Please also adjust the "(ii) NUMBER C	OF SEQUENCES:" response to include the skipped sequences.
8Skipped Sequences (NEW RULES)	Sequence(s) missing. If intent <210> sequence id number <400> sequence id number 000	ional, please insert the following lines for each skipped sequence
(NEW RULES)		cted in the Sequence Listing. 20>-<223> is MANDATORY if n's or Xaa's are present. ain location of n or Xaa, and which residue n or Xaa represents.
Response	Per 1.823 of Sequence Rules, the only scientific name (Genus/species). <220 is Artificial Sequence	valid <213> responses are: Unknown Artificial Sequence, or ><223> section is required when <213> response is Unknown or
11Use of <220>	Use of <220> to <223> is MANDATO "Unknown." Please explain source of g	0> "Feature" and associated numeric identifiers and responses. RY if <213> "Organism" response is "Artificial Sequence" or genetic material in <220> to <223> section. ol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
	resulting in missing mandatory numeric	ion of PatentIn version 2.0. This causes a corrupted file, a identifiers and responses (as indicated on raw sequence ager" or any other manual means to copy file to floppy disk.
13 Misuse of n/Xaa	"n" can only represent a single nucleoti	ide; "Xaa" can only represent a single <u>amino acid</u>
	AMC - Biotechnology System	ms Branch – 09/09/2003



IFWP

RAW SEQUENCE LISTING DATE: 09/29/2006
PATENT APPLICATION: US/10/593,659 TIME: 09:05:50

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L:17 M:271 C: Current Filing Date differs, Replaced Current Filing Date